

1 : NM_000787 . Homo sapiens
dopam...[gi:4503260]

PubMed, Protein, Related Sequences

LinkOut

LOCUS NM_000787 2725 bp mRNA PRI 19-MAR-1999
 DEFINITION Homo sapiens dopamine beta-hydroxylase (dopamine beta-monoxygenase) (DBH) mRNA.
 ACCESSION NM_000787
 VERSION NM_000787.1 GI:4503260
 KEYWORDS .
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2725)
 AUTHORS Kobayashi, K., Kurosawa, Y., Fujita, K. and Nagatsu, T.
 TITLE Human dopamine beta-hydroxylase gene: two mRNA types having different 3'-terminal regions are produced through alternative polyadenylation
 JOURNAL Nucleic Acids Res. 17 (3), 1089-1102 (1989)
 MEDLINE 89160241
 REFERENCE 2 (bases 1 to 2725)
 AUTHORS Nagatsu, T.
 TITLE Direct Submission
 JOURNAL Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry, Nagoya University, School of Medicine, Nagoya 466, Japan
 COMMENT REFSEQ: This reference sequence was derived from X13255.
 see also X13256 for type b mRNA
 Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50 (1988).
 PROVISIONAL RefSeq: This is a provisional reference sequence
 record that has not yet been subject to human review. The final curated reference sequence record may be somewhat different from this one.
 FEATURES Location/Qualifiers
 source 1..2725
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Figure 1A

EPFRSLEAINGSGLQMGLQRVQLLKPNIPEPELPSDACTMEVQAPNIQIPSQETTYWC
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siq peptide 33..107
mat peptide 108..1841
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 beta-monooxygenase)"

BASE COUNT 533 a 901 c 774 g 517 t
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Figure 1B

1801 ctgctggccc caccgttgtc agcattggtg gggcaaagg ctgagggggg acctactcct
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2641 ttcctgaccc tcactttct catctgtaaa accaggctga tgccgtgcgg gctaattgagc
2701 caataaagct cacacttggg ctggc

Figure 1C

SUMMARY OF DBH ASSOCIATION

Original study	Transmitted	Untransmitted	Chi-sq	p-val
DBHu2	20	21	0.53	0.4658
DBHu1	18	12	1.20	0.2733
DBHp444a	56	41	2.32	0.1278
Total⁴				
DBHu2	14	8	1.64	0.2008
DBHu1	11	13	0.17	0.6831
DBHp444a	49	38	1.39	0.2383
Replication/DePaulo				
DBHu2	40	29	1.75	0.1854
DBHu1	29	25	0.30	0.5882
DBHp444a	105	79	3.67	0.0553

DBH HAPLOTYPE ANALYSIS

Original Study	Transmitted	Untransmitted	Chi-sq	p-val
Allele1 from DBHu2 and u1	37	22	3.81	0.0508
Allele1 from DBHu2 and DBHp444a	45	29	3.40	0.0629
Allele1 from DBHu1 and DBHp444a	43	23	6.06	0.0138
Allele1 from all three SNPs	46	25	6.21	0.0127
Replication/DePaulo				
Allele1 from DBHu2 and u1	19	11	1.69	0.1936
Allele1 from DBHu2 and DBHp444a	32	14	7.04	0.0080
Allele1 from DBHu1 and DBHp444a	31	16	4.79	0.0287
Allele1 from all three SNPs	31	11	9.52	0.0020
Total⁵				
Allele1 from DBHu2 and u1	65	33	5.50	0.0190
Allele1 from DBHu2 and DBHp444a	77	43	9.63	0.0019
Allele1 from DBHu1 and DBHp444a	74	39	10.84	0.0010
Allele1 from all three SNPs	77	36	14.88	0.0001

FIG. 2